IN THE SPECIFICATION

Please replace the paragraph beginning at page 21, line 7 to page 22, line 17, with the following rewritten paragraph:

Hepatitis C is known to, for example, progress to cirrhosis and further to develop into liver cancer. As one of the treatments for hepatitis C, it is known to administer interferon (hereinafter referred to as "IFN"). IFN alpha and beta are often used for treatment. However, the efficacy of IFN greatly varies. For example, IFN effectively works on only about 20 to 30% of human patients of Japanese origin. Even when IFN works effectively, in a human patient, IFN has the problem of inducing extremely strong side effect in a human patient. Such a variance in efficacy of IFN is considered to be due to differences in the genotype of a hepatitis C virus (hereinafter referred to as "HCV") infecting a patient (see J. Clin. Microbiol., 34, 2516 (1996)) and the amount of virus, and difference in nucleic acid sequence of the patient infected with the virus. On the basis of comparison of nucleotide and predicted amino sequences of different regions of the HCV genome, at least six major genotypes have been reported (Forns et al., J. Clin. Microbiol., 34, 2516 (1996), Andonov et al., J. Clin. Microbiol., 33, 254 (1995). According to an aspect of the present invention, it is possible to estimate the efficacy of IFN against hepatitis C. The term "interferon (IFN)" used herein includes interferon α, β, γ and/or ω. For example, if the type of hepatitis C virus infecting a patient is Ib (the dominant type observed in Japan), IFN is less effective. It means that the concentration of HCV-RNA, HCV-antibody, GOP, and GTP in serum does not decrease by IFN treatment. However, if the type of virus is 2a, the efficacy of IFN is higher. It means that the concentration of HCV-RNA, HCV-antibody, GOP, and GTP in serum decrease by treatment. On the other hand, if the amount of virus is as large as [[106]] 10^6 copies/mL or more, the efficacy of IFN is low. Therefore, to check the genotype and

amount of virus infecting a patient at a nucleic acid level, the first probe according to the present invention is used.

Please replace the paragraph beginning at page 26, line 17 to page 27, line 5, with the following rewritten paragraph:

In the probe-immobilized chip of the present invention, if the aforementioned probe (SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7) is used as the first probe, it is possible to obtain information about the genotype of a pathogenic microorganism such as a virus infecting an individual, the amount of the virus, the presence of a site-specific mutation, and the quantity and ~~spiecies~~ species of an expressed gene. As a result, if the virus is a 1b genotype, which is dominantly observed in the Japanese patients, IFN works less effectively, whereas IFN works effectively if the virus is a 2a genotype. On the other hand, if the amount of virus is as large as [[106]] 10^6 copies/mL or more, the efficacy of IFN treatment can be estimated low. In this way, it is possible to estimate the efficacy of IFN treatment for an individual organism.

Please replace the paragraph beginning at page 30, line 22 to page 31, line 4, with the following rewritten paragraph:

IFN tends to act more effectively on a patient of a YA-YA homo-zygote type whose ~~MBL-211~~ MBL-227 position is type Y and alleles at codons 52, 54 and 57 are type A, compared to other types of patients, that is, YnonA-YA hetero and YnonA-YnonA homo-zygote types, whose MBL-211 position is type Y and alleles at codons 52, 54 and 57 are not type A. Conversely to say, IFN tends to act less effectively on the patients of YnonA-YA hetero and YnonA-YnonA homo-zygote types than the patient of a YAYA homo-zygote.

Please replace the paragraph beginning at page 34, line 25 to page 35, line 3, with the following rewritten paragraph:

The bases sequences represented by SEQ ID NOs: 16, 17, 18, 19, 37, 38, 39, and 40, each include a promoter region of a human MxA gene. Single ~~nucleopeptide~~ nucleotide polymorphism (SNP) present at the 455th position and 420th position of each of these base sequences is related to the efficacy of IFN treatment.

Please replace the two paragraphs beginning at page 36, line 2, with the following rewritten paragraphs:

Alternatively, compared to an HCV patient of T/non-T hetero or T/T homo, an HCV patient having a homologous zygote (referred to as "nonT/non-T homo") of promoter regions of an MxA gene where the 455 position is not thymine is less effectively treated with IFN. Examples of combinations of non-T/non-T homo are G/G, G/A, G/C, A/A, A/C, ~~A/C,~~ and C/C. Examples of combinations of T/non-T are T/G, T/A, and T/C.

The base sequence represented by SEQ ID NOS: 37-40 are identical except for the base of the ~~425th~~ 420th position. The ~~425th~~ 420th position of SEQ ID NO: 37 is ~~adenine~~ thymine. The ~~425th~~ 420th position of SEQ ID NO: 38 is ~~cytosine~~ guanine. The ~~425th~~ 420th position of SEQ ID NO: 39 is ~~thymine~~ adenine. The ~~425th~~ 420th position of SEQ ID NO: 40 is ~~guanine~~ cytosine.

Please replace the two paragraphs beginning at page 37, line 7, with the following rewritten paragraphs:

In the probe-immobilized chip of the present invention, if any one of the base sequence represented by SEQ ID NO: 17 containing an SNP site of guanine, a fragment of the base sequence, or any one of complementary sequences (ag455) to (eg455), the base

sequence represented by SEQ ID NO: 18 containing an SNP site of adenine, a fragment of the base sequence, or any one of complementary sequences (aa455) to (~~ee~~ ea455), and the base sequence represented by SEQ ID NO: 19 containing an SNP site having a base of adenine, a fragment of the base sequence, or any one of complementary sequences (ac455) to (ec455), is used as a second probe for use in detecting a sequence of a nucleic acid derived from an individual, it is possible to identify the base of the SNP site of the base sequence including the promoter region of a human MxA gene derived from an individual. In this way, the efficacy of IFN treatment for the individual can be estimated (see Japanese Patent Application Nos. 2001-62371 and 2001-62372).

Please replace the paragraph beginning on page 40, line 3 with the following replacement paragraph:

An HCV patient having a nucleic acid sequence represented by SEQ ID NO: [[37]] 39 where the ~~425th~~ 420th position is adenine is effectively treated with IFN, whereas an HCV patient ~~having no such a sequence of No. 37~~ not having SEQ ID NO: 39 is not effectively treated with IFN. The relationship between the sequence and the efficacy of IFN is almost the same as the case whether the SNP site is present at the 455th position.

Please replace the paragraph beginning at page 52, line 26 to page 53, line 15, with the following rewritten paragraph:

FIG. 1 shows a schematic view of a DNA chip according to Example 2. A substrate [[2]] 6 is a slide glass coated with polylysine. On the substrate [[2]] 6, second probes and first probes, each being 200 nL, were spotted and dried (in FIG. 1, the first and second probes are shown by reference numerals 1 to 5). In this case, the sequences represented by SEQ ID NO: 22, 23, 24, 25 and 26 were used as the second probe. The sequences represented by

SEQ ID NO: 5, 6, and 7 were used as the first probe. Thereafter, the DNA chip was irradiated with UV rays to immobilize the probes on the substrate [[2]] 6. The base sequences of SEQ ID NO: 22-25 were fragments of the base sequences represented by SEQ ID NO: 16-19, respectively, each having the SNP site of the 455th position. The base sequences of SEQ ID NO: 5-7 were probes used for detecting the genotypes of HCV viruses, namely, 1, 2, 3 types.

Please replace the paragraph beginning at page 54, line 9, with the following rewritten paragraph:

Example 3 describes a ~~PNR~~ PNA chip for estimating the efficacy of IFN treatment.

Please replace the paragraph beginning at page 56, line 20, with the following rewritten paragraph:

The flowchart for estimating the efficacy of IFN is started from Step 3a, where a specimen such as a blood specimen is taken from an individual to be treated with IFN. If necessary, the specimen thus taken may be purified by extraction or the like. Subsequently, a virus type and the genotypes of MxA-88, MxA-123, ~~MBL-211~~ MBL-227 and codon 54 of an MBL collagen like domain are determined.